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Patentanmeldung Nr. Patent application No. Demande de brevet n°

00114786.7

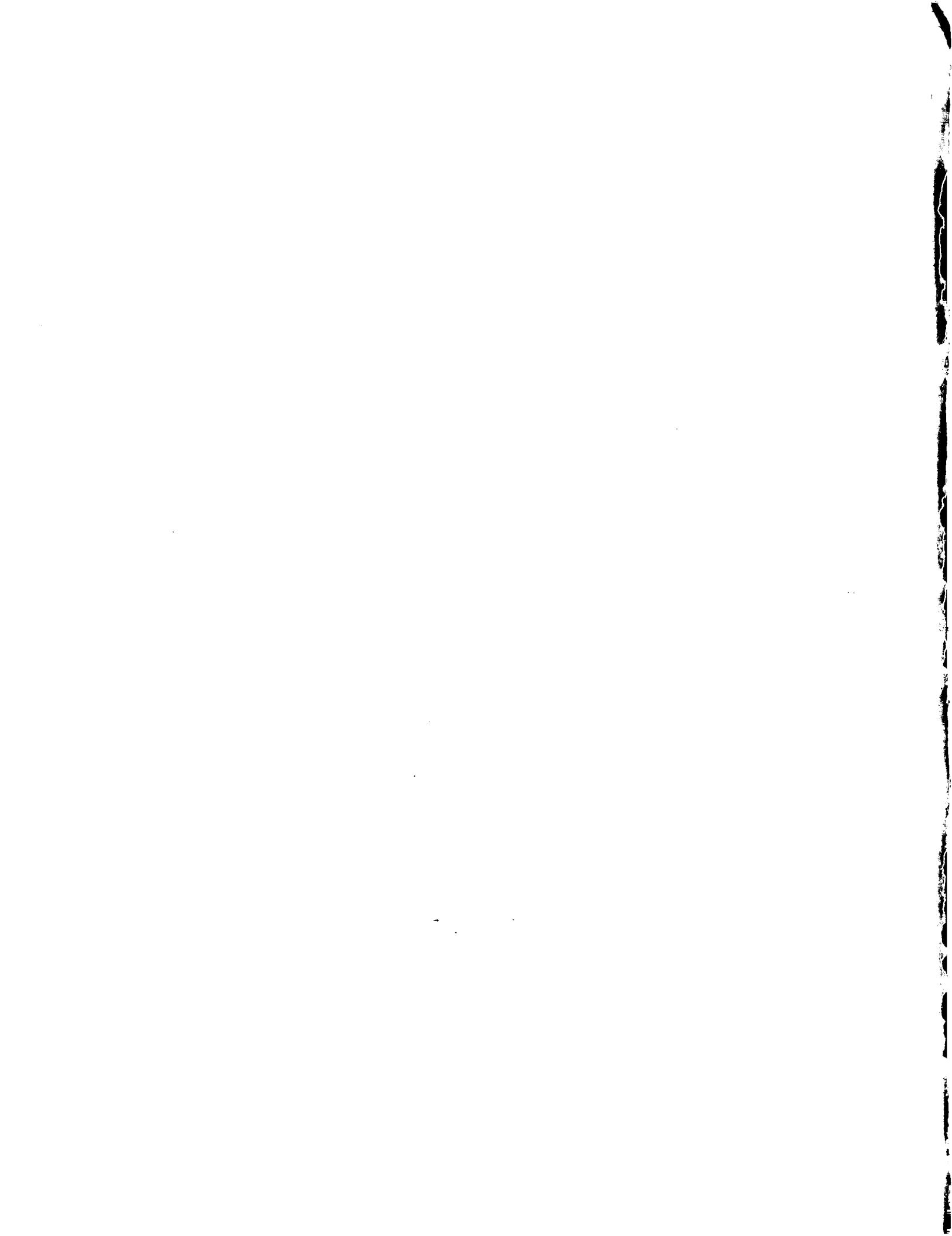
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Diagnostic use of polymorphisms in the gene coding for the TNF Receptor II and method for detecting non-responders to Anti-TNF therapy

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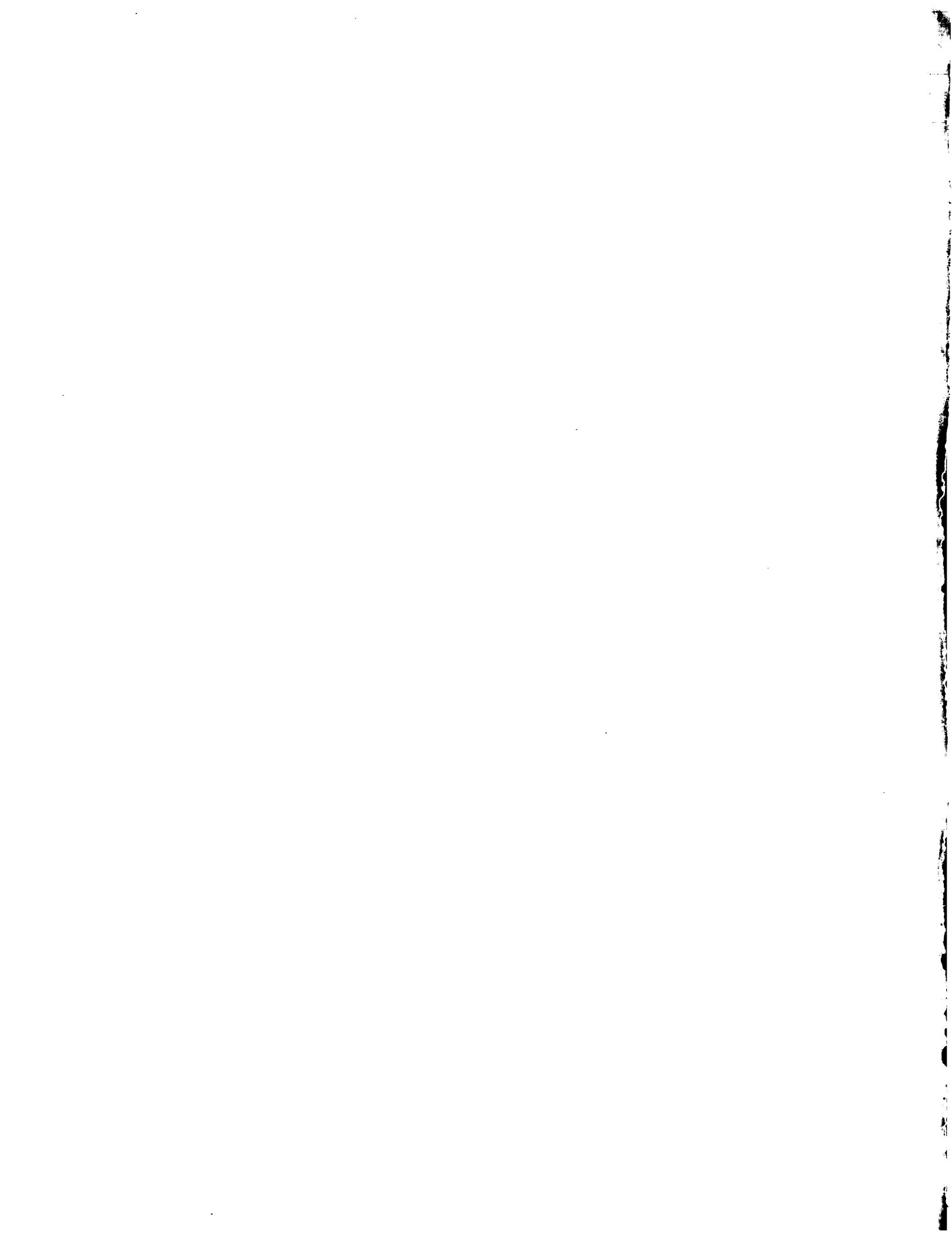
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Diagnostic Use of Polymorphisms in the
Gene Coding for the TNF Receptor II and
Method for Detecting Non-Responders to Anti-TNF Therapy

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The present invention relates to a method for detecting non-responders to anti-TNF therapy, the use of a novel polymorphism in exon 2 and a known polymorphism in exon 6 in the gene coding for the TNF Receptor II in anti-TNF therapy, to the genes containing the polymorphism in exon 2 or exons 2 and 6, and to the peptides encoded by the respective genes.

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Crohn's disease is a chronic inflammatory disorder of the intestine. It shares many clinical and pathophysiological characteristics with other autoimmune disorders including rheumatoid arthritis. A polygenic aetiology of Crohn's disease is strongly suspected (Hugo, J.P. et al. Mapping of a susceptibility locus for Crohn's disease on chromosome 16. *Nature* 379, 821-823 (1996); Cho, J. H. et al. Identification of novel susceptibility loci for inflammatory bowel disease on chromosome 1p. 3q. and 4q: Evidence for epistasis between 1p and IBD1. *PNAS* 95, 7502-7505 (1998); Satsangi J. et al. Two stage genome-wide search in inflammatory bowel disease provides evidence for susceptibility loci on chromosome 3, 7 and 12. *Nature Genet.* 14, 188-202 (1996); Hampe J. et al. A genomewide analysis provides evidence for novel linkages in inflammatory bowel disease in a large European cohort, *Am J Hum Genet* 64, 808-816 (1999)); Hampe J. et al. Linkage of Inflammatory bowel disease to human chromosome 6p. *Am J Hum Genet* 65, 1647-1655 (1999), although disease genes have not been identified yet.

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Glucocorticoids are an effective short term treatment of acute relapse in most patients. However, long term maintenance of remission is difficult in many patients. It is estimated that at least 50 % of patients develop a steroid refractory and dependent disease (Munkholm P., Langholz E., 5 Davisen M, Binder V. Frequency of glucocorticoid resistance and dependency in Crohn's disease. Gut 35, 360-362). An increased production of pro inflammatory cytokines including TNF- α (tumor necrosis factor α) in the intestinal mucosa is pivotal for the development of inflammatory relapses (Schreiber S. *et al.* Tumor necrosis factor alpha and interleukin 1 beta in relapse of Crohn's disease. Lancet 353, 10 459-461 (1999)) as well as chronic inflammatory activity.

The introduction of biological agents targeting TNF- α has led to impressive clinical results in therapy of refractory Crohn's disease.

15 Infliximab is a monoclonal antibody against TNF- α which was recently approved for therapeutic use in refractory and/or fistulating Crohn's disease in both the United States and Europe. Further, CDP571 and D2E7 are monoclonal antibodies directed against TNF- α with different 20 biological properties, which have either been engineered from murine antibody genes or were generated by the phage-display system, respectively. In addition, recombinant TNF-receptor based proteins have been developed (e.g. ethanercept). All bind specifically to human TNF- α (not TNF- β) but vary in their murine parts as well as the human subclass used. It is unclear whether other mechanisms in addition to neutralization 25 of TNF- α contribute to the therapeutic effect. It appears likely that at least infliximab can bind receptor attached or membrane expressed TNF- α and leads to deletion of activated immune cells either by complement activation or induction of apoptosis (Scallon B.J., Moore M.A., Trinh

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H., Knight D.M., Ghrayeb J., Chimeric anti-TNF-alpha monoclonal antibody cA2 binds recombinant transmembrane TNF-alpha and activates immune effector functions. *Cytokine* 7, 251-259 (1995)).

5 TNF Receptor I (CD120a) (Smith C.A., Farrah T., Goodwin R.G., *Cell* 76, 959-962 (1994); Baker S.J., Reddy E.P., *Oncogene* 12, 1-9 (1996)) is a 55/60 kDa (455 aa residues) transmembrane glycoprotein expressed in all nucleated mammalian cells. TNF Receptor II (CD120b) is a 75/80 kDa (461 aa residues) transmembrane glycoprotein expressed primarily by cells of the hematopoietic lineage and signals thymocyte and peripheral T-cells proliferation, natural killer cell and neutrophil activation. TNF Receptor II function is not completely known. Interaction between TNF- α and TNF Receptor II leads to a slow oligomerization of receptor molecules and ligand dissociation seems to occur before receptor-signalling complex formation. Membrane bound TNF- α seems to represent the effective ligand of TNF Receptor II. The mature human TNF Receptor II is a N and O glycosylated transmembrane protein.

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20 The gene coding for the TNF Receptor II (SEQ ID NO: 49) is located on chromosome 1p36 and consists of 10 exons and 9 introns (Santee S.M. and Owen-Schaub L.B. Human Tumor Necrosis Factor Receptor p75/80 (CD120b) gene structure and promoter characterization. *Journal Biological Chemistry* 271;21151-21159 (1996)). Comparison of TNF Receptor II sequences obtained by different groups has identified six potential single nucleotide polymorphisms (SNPs) in exon 4, exon 6, exon 9 and exon 10 (Pantelidis P., Lympnay P.A., Foley P.J., Fanning G.C. Welsh K.I. du Bois R.M. Polymorphic analysis of the high-affinity tumor necrosis factor receptor 2. *Tissue Antigens* 64: 585-591). In exon

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4 nucleotide substitutions at position 511-512 (all nucleotide positions refer to cDNA to mRNA sequence of GeneBank accession number M32315) give rise to an arginine to proline substitution at aa position 143; in exon 6 nucleotide substitution at position 676 corresponds to a metionine to arginine substitution at aa position 196; in exon 9 nucleotide substitution at position 1176 creates an alanine to threonine change at aa position 365; finally, the nucleotide substitution at positions 1663, 1668 and 1690 in the 3' untranslated region of exon 10. In addition to SNPs, were identified a (GATA)_n tetrameric repeat and a (GAA)(GGA) trimeric repeat in intron 1 (Santee S.M. and Owen-Schaub L.B. Human Tumor Necrosis Factor Receptor p75/80 (CD120b) gene structure and promoter characterization, Journal Biological Chemistry 271: 21151-21159 (1996)) and a (CA)₁₆ repeat in intron 4.

10 Previous studies suggest that polymorphisms in exons 6 and 10 of the gene coding for the TNF Receptor II, and amino acid exchange in TNF Receptor II potentially associated therewith, play a role in certain autoimmune diseases.

15 While polymorphisms in exon 4 and 9 have not been replicated, the ones in exon 6 and 10 have been studied in relation to several autoimmune diseases. Polymorphisms in exon 10 (3'UNR) at nucleotide positions 1663 and 1668 were tested in 90 patients with insulin dependent diabetes mellitus (IDDM), 101 with Graves' disease (GD) and 70 German healthy controls using Single Strand Conformation Polymorphism (SSCP) analysis (Rau H., Donner H., Usadel H. Badenhoop K. Polymorphisms of tumor necrosis factor receptor 2 are not associated with insulin-dependent diabetes mellitus or Graves' disease. Tissue antigens 49: 535-536 (1997)). Only one of the 2 polymorphic sites revealed 2 different

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alleles and no association was observed either with IDDM or GD in this German population. Contrasting results have been obtained for the coding mutation Met196Arg in exon 6 in relation to autoimmune diseases such as systemic Lupus erythematosus (SLE) and rheumatoid arthritis (RA). Met196Arg has been found not to be associated with RA in a Japanese population of 545 patients and 265 healthy controls (Shibue T. *et al.* Tumor necrosis factor alpha 5' flanking region, tumor necrosis factor receptor II, and HLA-DRB1 polymorphisms in Japanese patients with rheumatoid arthritis. *Tissue Antigens* 43(4): 753-757 (2000) 5
Rutgeerts Gastroenterolog 1999; 117: 761-69). In another Japanese population of 81 patients and 207 normal controls Arg196Met has been found associated with SLE (Komata T., Tsuchiya N., Matsushita M., Hagiwara K., Tokunaga K. Association of tumor necrosis factor receptor 10
2 (TNFR2) polymorphisms with susceptibility to systemic lupus erythematosus. *Tissue Antigens* 53: 527-533) but not in a cohort of 128 Spanish patients and 141 controls and in 74 UK patients and 90 controls (Al-Ansari A.S., Ollier W.E.R., Villarreal J., Ordl J. Teh L.S., Hajeer A.H. Tumor necrosis factor receptor II (TNFRII) exon 6 polymorphism 15
in systemic lupus erythematosus. *Tissue Antigens* 55: 97-99 (2000)).
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As regards Crohn's disease, a previous study in 193 Crohn's disease patients and 93 controls had suggested that polymorphism at position -308 in the TNF promoter might be related to disease localization and steroid dependency (Luis E. *et al.* Tumor necrosis factor (TNF) gene polymorphism in Crohn's disease (CD): influence on disease behaviour. *Clinical and Experimental Immunology* 199(1): 64-68 (2000)). The 25
microsatellite allele TNFa2 has been found associated with TNF- α and - β secretion in human mononuclear cells (Pociot *et al.* Association of tumor necrosis factor (TNF) and class II major histocompatibility

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complex alleles with the secretion of TNF-a and TNF-b by human mononuclear cells: a possible link to insulin-dependent diabetes mellitus. Eur J Immunol 23: 224-231 (1993)).

5 It has been outlined above that a new therapy against Crohn's disease involving the use of monoclonal antibodies directed against TNF- α has been developed. A one time infusion of the monoclonal antibody infliximab (commercially available as Remicade[®]) at a dose of 5-20 mg/kg bodyweight results in a remission rate of approximately 30-40% without statistical differences between dose groups (Targan S.R. et al. A short-term study of chimeric monoclonal antibody cA2 to tumor necrosis factor alpha for Crohn's disease. Crohn's disease cA2 Study Group. N Engl J Med 337, 1029-1035 (1997)). Although intensely investigated, clinical parameters (e.g. disease activity, which are related to the height of mucosal TNF- α production (Reinecker et al. Enhanced secretion of tumor necrosis factor-alpha, IL-6 and IL-1 by isolae lamina propria mononuclear cells from patients with ulcerative colitis and Crohn's disease, Clin Exp Immunol 94, 174-181 (1993)) could not be identified as predictors for responsiveness. Non-response appears to be a stable characteristic with patients staying non-responsive even if consecutive infusions are applied. The duration of response to a single dose anti TNF- α is variable with symptoms recurring in most patients after 6-12 weeks.

10 15 20 25 Infliximab infusions are generally well tolerated, although side effects resulting from intense immunosuppression have been described (including pneumonia, reactivation of intracellular infections, sepsis and abscess formation). In addition, 5 of about 600 patients (with rheumatoid arthritis and Crohn's disease) treated in clinical studies developed a malignant

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lymphoproliferative disease, and one more sporadic lymphoma has been reported in the more than 30,000 patients with Crohn's disease treated in the USA.

5 Taking into consideration that in only 30-40% of all patients receiving infliximab an alleviation of symptoms can be observed, it is a matter of fact that 60-70% of them receive infliximab without any therapeutic advantage but with the risk of potential severe side effects. Therefore, and also in view of the high price of biological therapeutics like infliximab, a possibility to predict, whether or not a specific patient suffering from Crohn's disease will respond to the therapy, would be highly desirable.

15 Therefore, it is an object of the present invention to provide a simple test for detecting non-responsiveness to anti-TNF therapy, in particular infliximab therapy, in a considerable percentage of non-responders.

20 It is a further object of the present invention to provide a polymorphism in a gene, which polymorphism, can be used for diagnostic purposes.

It is an additional object of the present invention to provide the use of a polymorphism in a gene for anti-TNF therapy or Crohn's disease.

25 It is also an object of the present invention to provide a genetic sequence containing at least one polymorphism rendering the gene suitable for diagnostic purposes.

The object is achieved by a method for detecting non-responders to anti-TNF therapy, comprising testing an individual for homozygosity for at

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least one single nucleotide polymorphism in the gene coding for the TNF Receptor II.

5 The object is also achieved by a novel single nucleotide polymorphism (SNP), a transition A to G, in position 257, or 168 from the transcription starting site, in exon 2 of the gene coding for the TNF Receptor II.

10 The object is further achieved by the use of the single nucleotide polymorphism (SNP), the transition T to G, in position 676, or 587 from the transcription starting site, in exon 6 of the gene coding for the TNF Receptor II.

15 The object is, in addition, achieved by the genes having the sequences identified in SEQ ID NO 51 and SEQ ID NO 53, and by nucleotide sequences coding for the same peptides or peptides having the same immunological properties.

20 The SNP in exon 2 corresponds to a silent mutation at amino acid position 56 (Lys56Lys), and the SNP in exon 6 corresponds to an amino acid change at position 196 (Met196Arg). Coupling analysis reveals that both SNPs are in strong linkage disequilibrium. Therefore, the SNP in exon 2 can be used as a marker for the SNP in exon 6.

25 It is a great advantage of the present invention that it can be accomplished with DNA which can be derived from any cell, e.g. blood cells or other cells or body fluids, e.g. saliva, or other body parts. Preferably, DNA is derived from EDTA-blood.

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It appeared likely to us that the differential response to infliximab represents a polygenic trait. Therefore, we decided to screen for mutations, by direct sequencing, the promoter, the 10 exons (including the 3'UNR) of the TNF Receptor II in 45 individuals of a study population consisting of 90 Crohn's disease patients and 180 controls, and then test the mutations present in the population, as well as known mutations in the TNF Receptor II and Receptor I, in a cohort of 90 Crohn's disease patients receiving infliximab.

5 3 fragments of the 5' regulatory region, the 10 exons and 1 fragment of the 3' untranslated region of the TNF Receptor II were direct sequenced in 45 individuals of the study population; the same primers, designed on the basis of the published sequence (Santee and Owen-Schaub, 1996), were used for PCR Amplification and sequencing: first fragment of the
10 5' regulatory region: forward primer 5'CTTCCACCGAGGTGACATCTCC3' (SEQ ID NO: 1), reverse primer 5'GCCCTAATACAGGGCCAGC3' (SEQ ID NO: 2), second fragment: forward primer 5'GGACAGATTGCAGCTGGAATG3' (SEQ ID NO: 3), reverse primer 5'TAGAGCCAGACCACCTGGGT3' (SEQ ID NO: 4);
15 third fragment: forward primer 5'AGCCTGGACAACATGGCGA3' (SEQ ID NO: 5), reverse primer 5'CCCTCGACTGAAAGCGAAAG3' (SEQ ID NO: 6); exon 1: forward primer (promoter) 5'GAGGCGTGTCCAAGGCC3' (SEQ ID NO: 7), reverse primer (intron 1) 5'GCGCGGAGTCACCACCT3' (SEQ ID NO: 8); exon 2: forward primer (intron 1) 5'ATCACCCATGGCAGAACCC3' (SEQ ID NO: 9), reverse primer (intron 2) 5'TGCCCTCACCCGGC3' (SEQ ID NO: 10); exon 3: forward primer (intron 2) 5'GACTCTGGCCTTGTTCCTCA3' (SEQ ID NO: 11), reverse primer (intron 3) 5'GGGAAGTTGGAGGCAGGG3' (SEQ ID NO: 12); exon 4:
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forward primer (intron 3) 5'TGACCGTTGCGCCCTC3' (SEQ ID NO: 13), reverse primer (intron 4) 5'GTCCCCAAGGACCTGAGCC3' (SEQ ID NO: 14); exons 5 and 6: forward primer (intron 4) 5'AGACAGAGCTCCTTGGC3' (SEQ ID NO: 15), reverse primer (intron 6) 5'GCAGACAGAACAGCAGTGAATGA3' (SEQ ID NO: 16); exons 7 and 8: forward primer (intron 6) 5'TCCTGGCTTGCTGGCTG3' (SEQ ID NO: 17), reverse primer (intron 8) 5'GAGGGCAGTGGAGACAC3' (SEQ ID NO: 18); exon 9: forward primer (intron 8) 5'GCTGACTGCTCTCCCCT3' (SEQ ID NO: 19), reverse primer (intron 9) 5'TGGGAAGAACAGCAGGTGTG3' (SEQ ID NO: 20); exon 10: forward primer (intron 9) 5'GAATCTGCATCTGGGCAGG3' (SEQ ID NO: 21), reverse primer (3' untranslated) 5'GAGGCTGCGGCTGTGGA3' (SEQ ID NO: 22); 3' untranslated region: forward primer 5'CGGTGTGGCTGTGTCGTA3' (SEQ ID NO: 23) and reverse primer 5'CCTACAGGGCTGCCACCTC3' (SEQ ID NO: 24). Direct sequencing was conducted using BigDye Terminator (PE Biosystems) and run on an automated sequencer ABI 310 (PE Biosystems).

Direct sequencing of the 3 regions of the promoter and of the 10 exons of the TNF Receptor II confirmed the polymorphisms at amino acid position 196 (exon 6), at nucleotide position 1663, 1668 and 1690 in the 3' UTR while the amino acid position 143 in exon 4 and the nucleotide positions -1413 and -1120 in the promoter did not appear polymorphic in the 45 individuals tested. The same applies to the polymorphism in exon 9. In addition, we identified a novel polymorphism, a transition (A to G) in the third codon position of amino acid 56 (Lysine) in exon 2 (nucleotide position 168 from the transcription starting site). This mutation appears to be in strong linkage disequilibrium with the Met196

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Arg in exon 6. On the basis of the data available in the literature and the results of our own sequencing we therefore decided to test in the cohort of patients receiving infliximab the following mutations: TNF Receptor I at promoter position -609 and in exon 1 at nucleotide position 36, corresponding to amino acid 12 (silent mutation); and TNF Receptor II in exon 2, silent mutation at amino acid position 56, further in exon 6, amino acid change at position 196 and in the 3' untranslated region in exon 10 at nucleotide position 1663 and 1690.

5 An open label, prospective multicenter clinical trial, which was conducted in 31 German centers, was specifically set up for the evaluation of pharmacogenomics and biological markers of response. Inclusion criteria (steroid/azathioprine refractory Crohn's disease, stable co-medication before and throughout the study) were similar to those used in previously published studies which established the clinical efficacy of infliximab in Crohn's disease (Present D.H. *et al*/Infliximab for the Treatment of Fistulas in Patients with Crohn's Disease N. Eng J Med 340(18): 1398-405 (1999); Targan S.R. *et al*. A short-term study of chimeric monoclonal antibody cA2 to tumor necrosis factor alpha for Crohn's disease. Crohn's disease cA2 Study Group. N Engl J Med 337, 1029-1035 (1997). The trial was conducted and monitored according to the standards of "Good Clinical Practice" (GCP). The protocol and the genetic test procedures received prior approval by all local ethics committees/institutional review boards. 96 patients with moderate to severe steroids refractory or steroid dependent Crohn's disease (10 mg or more/day) active for at least six months, with CDAI between 220 and 450, decided to participate in the treatment protocol and to provide EDTA (ethylene diamine tetraacetic acid) blood for DNA based analysis after written informed consent. At the time of the analysis clinical data

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was missing for 6 patients leaving the study cohort to 90 patients (55 women and 33 men and 2 unknown). The overall remission rate (as indicated by a Crohn's disease activity index below 150 points) (38 % at 4 weeks) was in the range as expected by previous studies (Targan S.R. *et al.* A short-term study of chimeric monoclonal antibody cA2 to tumor necrosis factor alpha for Crohn's disease. Crohn's disease cA2 Study Group. *N Engl J Med* 337, 1029-1035 (1997); Schraub L.B. Human tumor necrosis factor receptor p75/80 (CD120b) gene structure and promoter characterisation. *J. Biol. Chemistry* 271, 21151-21159 (1996)).

5 On enrolment in the trial EDTA blood was obtained from each patient as well as from 180 German blood donors as normal controls. DNA was extracted by standard techniques (e.g. using DNAzol based on a guanidine-detergent lysing solution) and dispensed on 96 well plates (20 ng/well).

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15 6 SNPs were genotyped using TaqMan (ABI 7700 PE Biosystems, Foster City, CA) allelic discrimination: 2 SNPs in the TNF Receptor I gene (12p13), one in the promoter at position -609 from the transcription starting site and one in exon 1, a silent mutation at amino acid position 12, Pro12Pro (CCA-CCG) and 4 SNPs in the TNF Receptor II gene (1p36), a silent mutation in exon 2 at amino acid position 56, Lys56Lys (AAA-AAG), a second codon position in exon 6 changing amino acid 196, Met196Arg (ATG-AGG), and 2 mutations in exon 10 in the 3' untranslated region at nucleotide position 1663 and 2007. Genotypes were assigned without knowledge of treatment response. Primers and probes (see table 1) were designed using Primer Express (PE Biosystems) and purchased from Eurogentec. PCR amplification was conducted with the termocycler 9700 (PE Biosystems) in a final volume of 10 μ l. The amplification conditions involved two pre-PCR steps of 2

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min at 50°C and 10 min at 95°C followed by a variable number of cycles including a denaturation step at 95°C for 15 sec and an annealing step of 1 min at different temperatures for the different assays (see table 2).

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While TaqMan allelic discrimination is an approved technique, the present invention should not be regarded as being limited thereto. The genotype may as well be determined by direct sequencing, RFLP (restriction fragment length polymorphism), PCR (polymerase chain reaction) - based techniques or any other technique or combination of techniques known to those skilled in the art for identifying a specific mutation.

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A further particularly suitable procedure is PCR followed by restriction digestion with NlaIII \downarrow 5'CAGT \uparrow 3' (commercially available from New England Biolabs with catalogue number #125S or #125L. This enzyme cuts at position 277, 677, 941 etc. Regarding the exon 6-polymorphism, primers between 278 and 940 will yield one cut in the wild type and no cut in the mutant.

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PCR-SSCP with 3' mismatches in forward and reverse primers was described in Pentelidis et al., Tissue antigens 54: 585-591 (1999) for the mutation in exon 6 as well as for exons 4, 9 and 10.

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The genotypes obtained by TaqMan were checked by direct sequencing in 45 individuals of the study population obtaining in every case identical result.

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Table 1: TaqMan primers and probes:

	<u>TNF-R1 promoter -609 (G/T)</u>
	FAM probe (G allele)
5	5'ACAGATCCAGACAGGTTCAGTTATGTGTCTGAGAAGTT3' (SEQ ID NO: 25)
	TET probe (T allele)
	5'ACAGATCCAGACAGTTCAGTTATGTGTCTGAGAAGTT3' (SEQ ID NO: 26)
10	Forward primer 5'GACAGGTTATCTCCACTCTGCAAA3' (SEQ ID NO: 27)
	Reverse primer 5'CAATTAGAATGCTTAGCTTTAGC3' (SEQ ID NO: 28)
15	<u>TNF-R1 Exon1 Pro12Pro (A/G)</u>
	FAM probe (G allele) 5'TGCTGCTGCCGCTGGTGAGACC3' (SEQ ID NO: 29)
20	TET probe (A allele) 5'AACTGCTGCTGCCACTGGTGAGACC3' (SEQ ID NO: 30)
	Forward primer 5'CTTGGGACGTCCCTGGACAGAC3' (SEQ ID NO: 31)
	Reverse primer 5'AAGGTGCCTCGCCCCACC3' (SEQ ID NO: 32)
25	<u>TNF-R2 Exon2 Lys56Lys (A/G)</u>
	FAM probe (A allele) 5'TGCAGCAAATGCTCGCCGGT3' (SEQ ID NO: 33)

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TET probe (G allele) 5'TGCAGCAAGTGCTCGCCGGG3' (SEQ ID NO: 34)

Forward primer 5'CAGAGAATACTATGACCAGACAGCTCA3 (SEQ ID NO: 35)

5 Reverse primer 5'GAGTGCCCCGTGGCT3' (SEQ ID NO: 36)

TNF-R2 Exon6 Met196Arg (T/G)

10 FAM probe (T allele) 5'AATGCAAGCATGGATGCAGTCTGCAC3' (SEQ ID NO: 37)

TET probe (G allele) 5'AATGCAAGCAGGGATGCAGTCTGCAC3' (SEQ ID NO: 38)

Forward primer 5'GCTGTAACGTGGTGGCCATC3' (SEQ ID NO: 39)

Reverse primer 5'CTGGGTTCTGGAGTT3' (SEQ ID NO: 40)

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TNF-R2 3'UNT nt 1663 (G/A)

20 FAM probe (A allele) 5'AGAGGCAGCGAGTTGTGGAAAGCCTC3' (SEQ ID NO: 41)

TET probe (G allele) 5'AGGCAGCGGGTTGTGGAAAGCCT3' (SEQ ID NO: 42)

Forward primer 5'ACCACTAGGACTCTGAGGCTCTTC3' (SEQ ID NO: 43)

Reverse primer 5'CCAGCCAGCCTCCGAG3' (SEQ ID NO: 44)

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TNF-R2 3'UNT nt 1690 (T/C)

FAM probe (C allele) 5'CCTCTGCTGCCATGGCGTGTCC3' (SEQ ID NO: 45)

5 TET probe (T allele) 5'CCTCTGCTGCCATGGTGTGTCCT3' (SEQ ID NO: 46)

Forward primer 5'CTGCAGGCCAAGAGCAGAG3' (SEQ ID NO: 47)

Reverse primer 5'GGTTTTCTGGAAGGCCAGAGCT3' (SEQ ID NO: 48)

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	SNP position	FAM Probe	TET Probe	Forward Primer	Reverse Primer	Annealing temperature and time	N. of cycles
15							
20	TNF-R1 Promoter-609	200 nM	200 nM	300 nM	300 nM	1 min 64°C	55
	TNF-R1 Exon 1 Pro12Pro	200 nM	200 nM	300 nM	300 nM	1 min 60°C	50
	TNF-R2 Exon 2 Lys56Lys	200 nM	200 nM	900 nM	900 nM	1 min 60°C	40
	TNF-R2 Exon 6Met196Arg	100 nM	100 nM	50 nM	900 nM	1 min 62°C	50
	TNF-R2 3'UNT nt 1663	200 nM	200 nM	300 nM	300 nM	1 min 60°C	50
25	TNF-R2 3'UNT nt 1690	200 nM	200 nM	50 nM	900 nM	1 min 60°C	50

Table 2: Probes and primers concentrations and amplification conditions for TaqMan assays (ABI 7700).

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Of the 6 mutations tested only the one in exon 6 of the TNF Receptor II leads to an amino acid exchange (Met→ Arg at amino acid position 196). Exon 6 codes a small portion of the transmembrane region and part of the extracellular domain including the proteolytic cleavage site that produces the soluble form of TNF Receptor II. Amino acid 196 is

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located within the extracellular region near one of the two N-glycosylation sites. It appears to be positioned at the border of the area for which the receptor structure can be predicted and it may have a possible influence on receptor conformation (Zimmer, Lengauer, personal communication). Presently, it is not certain whether this mutation has a functional significance.

The allele and genotype frequency in the controls were comparable to the ones obtained by Ansari in Spanish and UK populations outlined above. Within our patient population, for the mutation in exon 6 there were 61 (67.8%) homozygote wild type, 23 (25.5 %) heterozygote and 6 (6.7 %) homozygote mutant. For the mutation in exon 2 there were 58 (64.4 %) homozygote wild type, 25 (27.8 %) heterozygote and 7 (7.8 %) homozygote mutant (table 3).

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		Patients (total 90)	Controls (total 180)
Genotype frequency			
20	Met196 (wild type)	0.678 (61)	0.672 (121)
	Met196Arg (heterozygote)	0.255 (23)	0.300 (54)
25	Arg196 (mutant)	0.067 (6)	0.028 (5)
Allele frequency			
30	Met196 (wild type)	0.805	0.821
	Arg106 (mutant)	0.195	0.179

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Table 3: Genotype and allele frequency of the Met196Arg among the 90 infliximab treated patients and 180 controls (from sex matched healthy blood donors recruited from the German population).

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TaqMan results were checked by direct sequencing in 45 individuals.

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It was found that homozygosity for the single nucleotide polymorphism in exon 6 is always associated with non-response to infliximab (i.e. neither reaching clinical improvement (drop of the CDAI by at least 70 points) nor remission (CDAI < 150 points) resulting in a test specificity of 100 % in these individuals (table 4). Homozygote individuals show a marked reduction in clinical improvement (as indicated by a significantly smaller drop in the Crohn's disease activity index) after treatment with infliximab whereas a heterozygous genotype was not associated with an altered clinical response (table 4), i.e. the observed differences between homozygote and heterozygote individuals were at a statistically not significant level. The single nucleotide polymorphism at amino acid 196 (exon 6) of TNF Receptor II leads to a non-conservative amino acid substitution between Met(ATG) and Arg(AGG). About 10 % of non-responders are characterized by this genetic variation.

15

20

- 19 -

	5	Response 70 points (after 4 weeks)	Response 100 points (after 4 weeks)	Clinical remission (after 4 weeks)			
				Yes	No	Yes	No
	10	Met196 (wild type)	36 25	32	29	18	42
		61 patients					1 not known
		Heterozygote	17 6	13	10	11	12
		23 patients					
		Arg 196 (mutant)	0 6	0	6	0	6
	15	6 patients					

Table 4: Distribution of exon 6 genotype frequency among responders and not responders after 4 weeks from the infliximab infusion. The response has been evaluated as reduction of CDAI of 70 points, 100 points and as clinical remission (CDAI less than 150 points)

20 The Crohn's disease activity index incorporates 8 variables related to the disease activity: the number of liquid or very soft stools, the severity of abdominal pain or cramping, general well-being, the presence of extra-intestinal manifestations, abdominal mass, use of antidiarrheal drugs, haematocrit and body weight. These items yield a composite score ranging from 0 to approximately 650. Higher scores indicate greater disease activity. Scores below 150 are compatible with remission, whereas scores above 550 indicate severe illness.

25 30 By testing patients suffering from Crohn's disease before treatment with infliximab for the mutation in exon 6, at least 10 % of those which will

- 20 -

not respond can be detected in advance and be excluded from the useless therapy.

5 A second mutation in the same gene, the silent mutation in exon 2, is in a high degree of linkage disequilibrium, i.e. in almost complete linkage disequilibrium (4 discordant genotypes out of 90, i.e. there was 1 genotype heterozygote for the mutation in exon 6 and homozygote mutant for the mutation in exon 2, and 3 genotypes homozygote wild type for the mutation in exon 6 and heterozygote for the mutation in exon 2.) with the polymorphism in exon 6. Again, homozygotes are completely non-responsive to anti-TNF treatment with infliximab.

10

Therefore, the mutation in exon 2 can be used as a marker, to detect the same non-responders as the test for the exon 2 polymorphism.

15

In the TNF Receptor I gene no mutations were detected with an influence on the amino acid sequence (table 5). None of the mutations was in linkage disequilibrium with the mutation in exon 6 of the TNF Receptor II and no association with a therapeutic response was seen.

20

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- 21 -

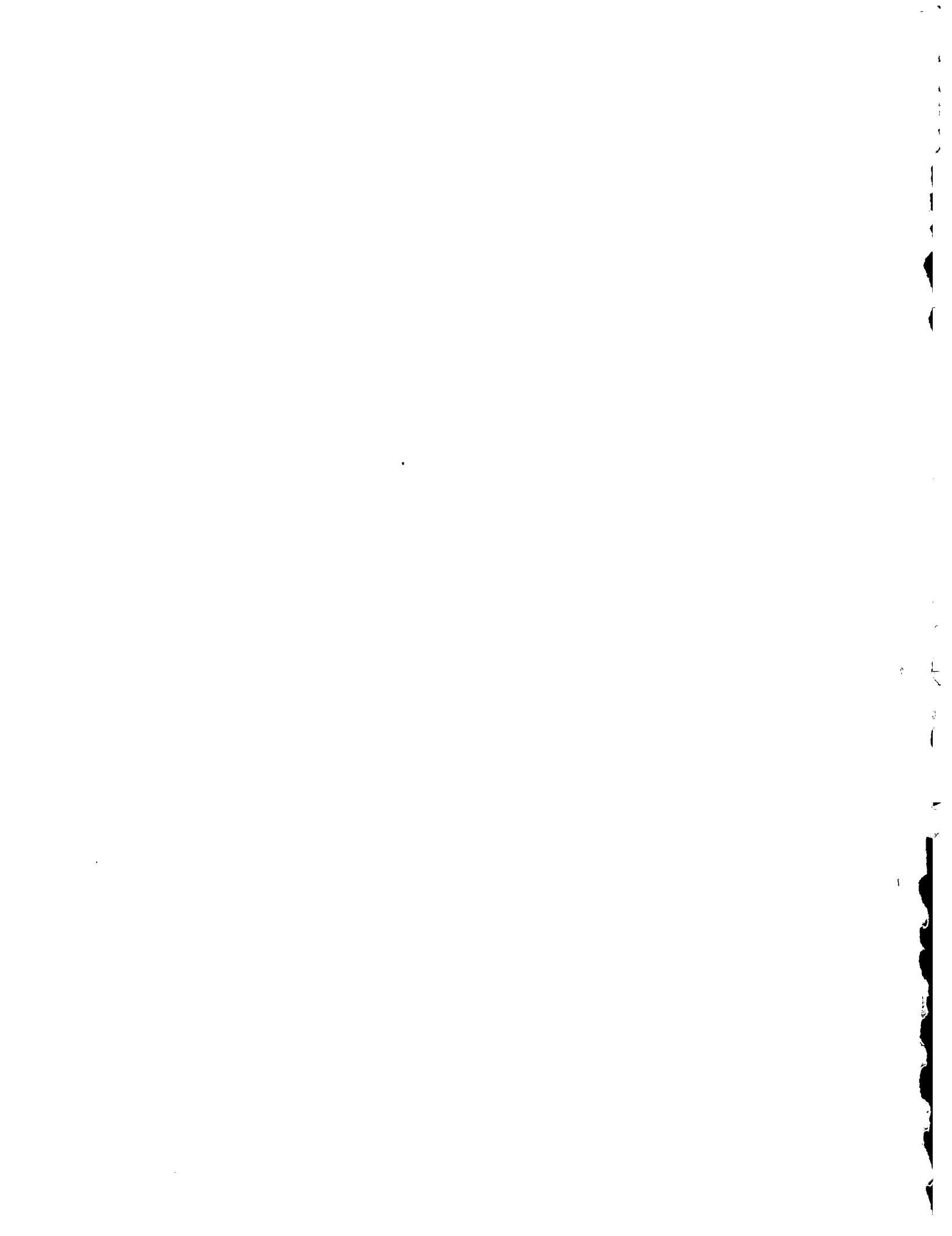
5	Gene and chromosomal localisation	Localisation and characteristics of the mutations:
10	TNF Receptor I (p55) chromosome 12p13*** **	Promoter -609 Pro12Pro (Pro CCA-CCG) (nucleotide position +36 MspA1, extracellular domain)
15	TNF Receptor II (p75) chromosome 1p36	Lys56Lys (exon 2) Met196Arg (exon 6, extracellular domain) 2 mutations in the 3'UNT region

Table 5: Mutations tested and gene localisation

** (Weinshenker et al., Neurology 52, 1500-1503 (1999))

*** Fuchs Peter, Strehl Sabine, Dworzak Michael, Himmller Adolf and Ambors Peter Structure of the Human TNF Receptor 1 (p60) Gene (TNFR1) and Localisation to Chromosome 12p13. *Genomics* (1992) 13:219-224

25 The effect of the polymorphism at position 168 in exon 2 has been shown exemplarily for Crohn's disease. The applicability of this polymorphism, however, is not restricted to Crohn's disease, but extends to any disease wherein TNF α plays a role, in particular inflammatory or malignant diseases.



SEQUENCE LISTING

EPO - Munich

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09. Juli 2000

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the TNF Receptor II and Method for Detecting
Non-Responders to Anti-TNF-Therapy

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 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
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 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
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 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
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 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
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 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
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 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
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 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
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 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
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 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
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 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
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<210> 51

<211> 3683

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(1475)

<220>

<221> mat_peptide

<222> (156)

<400> 51

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 Met Ala Pro Val Ala Val Trp Ala
 -20 -15

gcg ctg gcc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
 -10 -5 -1 1

gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc 209
 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
 5 10 15

cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aag 257
 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
 20 25 30

tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
 35 40 45 50

acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
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tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401

Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln			
70	75	80	
gtg gaa actcaa gcc tgc actcg gaa cag aac cgc atctgc acc tgc	449		
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys			
85	90	95	
agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg	497		
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu			
100	105	110	
tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca	545		
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro			
115	120	125	130
gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg	593		
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr			
135	140	145	
tcc tcc aac acg act tca tcc acg gat att tgc agg ccc cac cag atc	641		
Phe Ser Asn Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile			
150	155	160	
tgt aac gtg gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc	689		
Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys			
165	170	175	
acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta	737		
Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu			
180	185	190	
ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa	785		
Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu			
195	200	205	210
ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc	833		
Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser			
215	220	225	
ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca gtt gga ctg	881		
Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu			
230	235	240	
att gtg ggt gtg aca gcc ttg ggt cta cta ata ata gga gtg gtg aac	929		
Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn			
245	250	255	
tgt gtc atc atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga	977		

Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg
 260 265 270

 gaa gcc aag gtg cct cac ttg cct gcc gat aag gcc cgg ggt aca cag 1025
 Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln
 275 280 285 290

 ggc ccc gag cag cag cac ctg ctg atc aca gcg ccg agc tcc agc agc 1073
 Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser
 295 300 305

 agc tcc ctg gag agc tcg gcc agt gcg ttg gac aga agg gcg ccc act 1121
 Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr
 310 315 320

 cgg aac cag cca cag gca cca ggc gtg gag gcc agt ggg gcc ggg gag 1169
 Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
 325 330 335

 gcc cgg gcc agc acc ggg agc tca gat tct tcc cct ggt ggc cat ggg 1217
 Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Pro Gly Gly His Gly
 340 345 350

 acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac 1265
 Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp
 355 360 365 370

 cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca 1313
 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
 375 380 385

 gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc 1361
 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
 390 395 400

 aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca gag acc ctg 1409
 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
 405 410 415

 ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct 1457
 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
 420 425 430

 ggg atg aag ccc agt taa ccaggccggt gtgggctgtg tcgttagccaa 1505
 Gly Met Lys Pro Ser
 435 440

 ggtgggctga gccctggcag gatgaccctg cgaaggggcc ctggtccttc caggccccca 1565

ccactaggac tctgaggc tc ttctggcc aagttcctct agtgcctcc acagccgcag 1625
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 gtgttgcgtg tcgtgggtgt gtgttagccaa ggtcggtaaat ttgaatggcc tgccttgaag 2945
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<211> 461
<212> PRT
<213> *Homo sapiens*

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 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
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 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430
 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445
 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

<210> 53
 <211> 3683
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (90)..(1475)

<220>

<221> mat_peptide

<222> (156)

<400> 53

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 Met Ala Pro Val Ala Val Trp Ala
 -20 -15

gcg ctg gcc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
 -10 -5 -1 1

gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc 209
 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
 5 10 15

cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aag 257
 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
 20 25 30

tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
 35 40 45 50

acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
 55 60 65

tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401
 Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
 70 75 80

gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc 449
 Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
 85 90 95

agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg 497
 Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu
 100 105 110

tgc	gct	ccg	ctg	cgc	aag	tgc	cgc	ccg	ggc	ttc	ggc	gtg	gcc	aga	cca	545
Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
115			120							125				130		
gga	act	gaa	aca	tca	gac	gtg	gtg	tgc	aag	ccc	tgt	gcc	ccg	ggg	acg	593
Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
135			140							140			145			
ttc	tcc	aac	acg	act	tca	tcc	acg	gat	att	tgc	agg	ccc	cac	cag	atc	641
Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
150									155				160			
tgt	aac	gtg	gtg	gcc	atc	cct	ggg	aat	gca	agc	agg	gat	gca	gtc	tgc	689
Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Arg	Asp	Ala	Val	Cys	
165			170						175							
acg	tcc	acg	tcc	ccc	acc	cg	agt	atg	gcc	cca	ggg	gca	gta	cac	tta	737
Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
180			185						190							
ccc	cag	cca	gtg	tcc	aca	cga	tcc	caa	cac	acg	cag	cca	act	cca	gaa	785
Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
195			200						205				210			
ccc	agc	act	gct	cca	agc	acc	tcc	ttc	ctg	ctc	cca	atg	ggc	ccc	agc	833
Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
215			220						225							
ccc	cca	gct	gaa	ggg	agc	act	ggc	gac	ttc	gct	ctt	cca	gtt	gga	ctg	881
Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
230			235						240							
att	gtg	ggt	gtg	aca	gcc	ttg	ggt	cta	cta	ata	ata	gga	gtg	gtg	aac	929
Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
245			250						255							
tgt	gtc	atc	atg	acc	cag	gtg	aaa	aag	aag	ccc	ttg	tgc	ctg	cag	aga	977
Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
260			265						270							
gaa	gcc	aag	gtg	cct	cac	ttg	cct	gcc	gat	aag	gcc	cgg	ggt	aca	cag	1025
Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
275			280						285				290			
ggc	ccc	gag	cag	cac	ctg	ctg	atc	aca	gct	ccg	agc	tcc	agc	agc	1073	
Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser		
295			300						300			305				

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 Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr
 310 315 320

cgg aac cag cca cag gca cca ggc gtg gag gcc agt ggg gcc ggg gag 1169
 Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
 325 330 335

gcc cgg gcc agc acc ggg agc tca gat tct tcc cct ggt ggc cat ggg 1217
 Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Pro Gly Gly His Gly
 340 345 350

acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac 1265
 Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp
 355 360 365 370

cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca 1313
 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
 375 380 385

gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc 1361
 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
 390 395 400

aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca gag acc ctg 1409
 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
 405 410 415

ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct 1457
 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
 420 425 430

ggg atg aag ccc agt taa ccaggccggt gtgggctgtg tcgttagccaa 1505
 Gly Met Lys Pro Ser
 435 440

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tgtttgtttt aaaaaaaaaa 3683

<210> 54
<211> 461
<212> PRT
<213> *Homo sapiens*

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 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220
Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
260 265 270
Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
275 280 285
Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
290 295 300
Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305 310 315 320
Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
325 330 335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
340 345 350
Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365
Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380
Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400
Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430
Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460

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Claims

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1. A method for detecting non-responders to anti-TNF therapy, comprising testing an individual for homozygosity for at least one single nucleotide polymorphism in the gene coding for the TNF Receptor II.

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2. The method of claim 1, wherein anti-TNF therapy is infliximab therapy.

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3. The method of claim 1 or 2, wherein anti-TNF therapy is therapy of Crohn's disease.

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4. The method of any one of claims 1 to 3, wherein the at least one single nucleotide polymorphism is nucleotide substitution T/G at position 587 from the transcription starting site in exon 6 of the gene coding for the TNF Receptor II.

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5. The method of any one of claims 1 to 4, wherein the at least one single nucleotide polymorphism is nucleotide substitution A/G at position 168 from the transcription starting site in exon 2 of the gene coding for the TNF Receptor II.

6. The method of claim 4 or 5, comprising identifying the mutation A/G at position 168 and/or the mutation T/G at position 587 by a technique suitable therefor.

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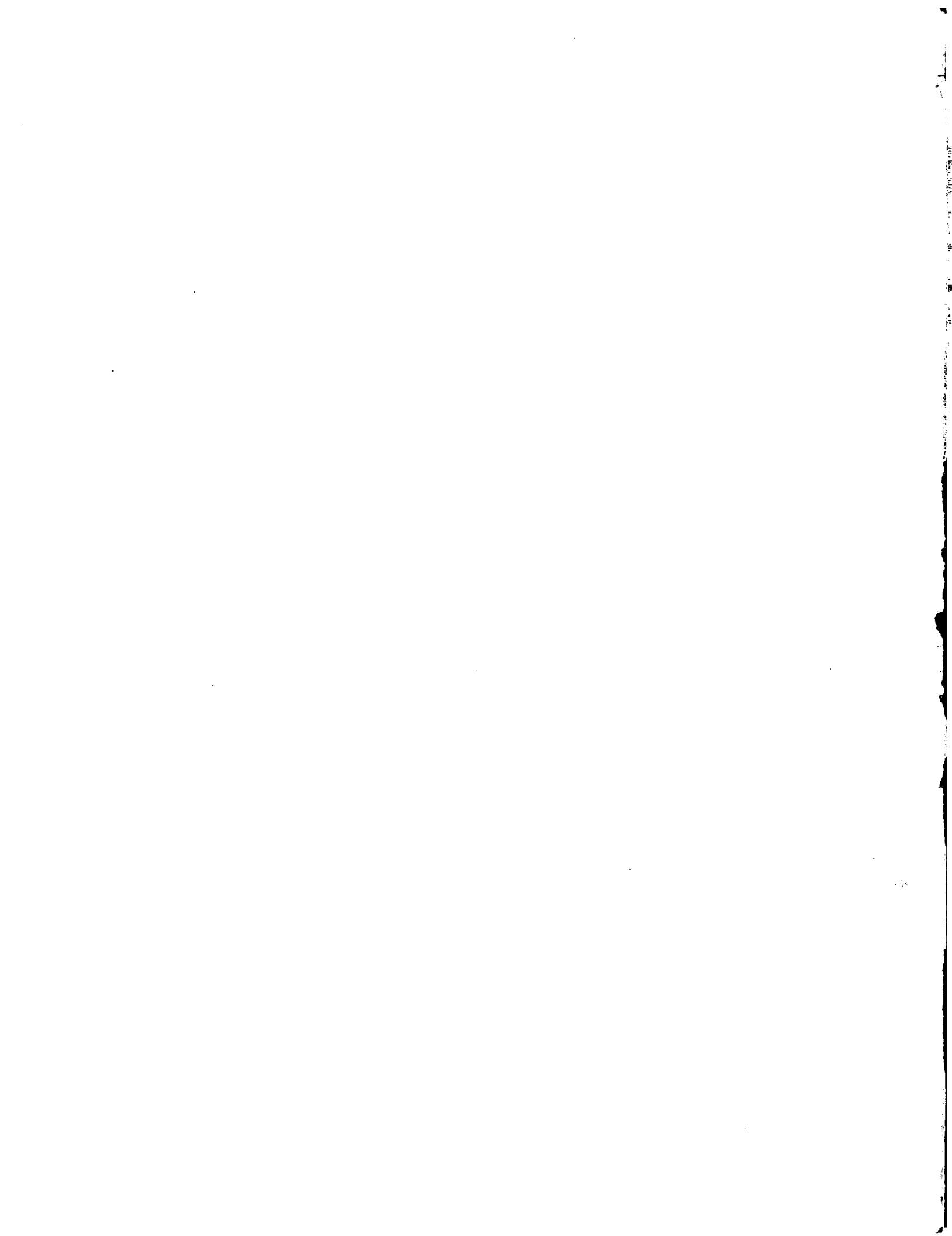
7. The method of any one of claims 1 to 7, comprising the use of blood cells for providing DNA.
- 5 8. Use of a polymorphism at position 168 (A/G) in exon 2 of the gene coding for the TNF Receptor II for diagnostic purposes.
9. The use of claim 8 in an inflammatory or malignant or other chronic disease.
- 10 10. The use of claim 9 in Crohn's disease.
11. The use of any one of claims 8 to 10 in anti-TNF therapy.
- 15 12. Use of a polymorphism at position 587 (T/G) in exon 6 of the gene coding for the TNF Receptor II in Crohn's disease.
13. Use of a polymorphism at position 587 (T/G) in exon 6 of the gene coding for the TNF Receptor II in anti-TNF therapy.
- 20 14. A kit comprising reagents tailored to identify the polymorphism at position 168 (A/G) in exon 2 and/or the polymorphism at position 587 (T/G) in exon 6 of the gene coding for the TNF-Receptor II.
- 25 15. Gene having the nucleotide sequence identified in SEQ ID NO 51 or a nucleotide sequence coding for the same peptide or a peptide having the same immunological properties.

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16. Gene having the nucleotide sequence identified in SEQ ID NO 53 or a nucleotide sequence coding for the same peptide or a peptide having the same immunological properties.
- 5 17. Peptide having the sequence identified in SEQ ID NO 52 or a peptide having the same immunological properties.
18. Peptide having the sequence identified in SEQ ID NO 54 or a peptide having the same immunological properties.

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Abstract

The invention relates to a method for detecting non-responders to anti-TNF therapy comprising testing an individual for homozygosity for a single nucleotid polymorphism in the gene coding for the TNF Receptor II. Monoclonal antibodies against TNF- α (infliximab) represent a new treatment for steroid refractory Crohn's disease that result in a remission rate of 30-50% after 4 weeks. Known single nucleotid polymorphisms within the TNF Receptor I and TNF Receptor II were tested for association with the response to the therapy. It was found that individuals homozygote for the mutated allele arginine at amino acid position +196 in the TNF Receptor II or the mutated allele in exon 2 at amino acid position 56 did not respond. Polymorphisms in exon 2 was newly found. None of the individuals homozygote for the mutations in exons 2 or 6 responded. The mutation in exon 2, although a silent mutation, can be used as a marker because it is in a high linkage disequilibrium with the mutation in exon 6.

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